



096429-9141.ST25.txt  
SEQUENCE LISTING

<110> Welch, Rodney A.  
Lathem, Wyndham W.  
Grys, Thomas E.

<120> E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE

<130> 096429-9141

<140> Current Application Number: US/10/786,445

<141> 2004-02-25

<150> 10/002,309

<151> 2001-10-26

<150> 60/243,675

<151> 2000-10-26

<160> 25

<170> PatentIn version 3.1

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&lt;222&gt; (138)..(2798)

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## 096429-9141.ST25.txt

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Page 7

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505

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Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg Leu Ala Asn His Arg  
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gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat      218
Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn
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tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt      266
Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly
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tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc      314
Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala
                45                50                55

cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa      362
His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys
        60                65                70                75

agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt      410
Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val
                80                85                90

cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc      458
Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr
                95                100                105

ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt      506
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gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag      554
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## 096429-9141.ST25.txt

Ile 140	Ile	Asn	Thr	Val	Ala 145	Glu	Val	Asn	Lys	Leu 150	Ser	Asp	Ala	Ser	Gly 155	
agt Ser	tct Ser	att Ile	cat His	agc Ser 160	cat His	cta Leu	aca Thr	aat Asn	aat Asn 165	gca Ala	ctg Leu	gtg Val	gag Glu	atc Ile 170	cat His	650
act Thr	gca Ala	aat Asn	ggg Gly 175	cgt Arg	tgg Trp	gta Val	aga Arg	gac Asp 180	att Ile	tat Tyr	ctg Leu	ccg Pro	cag Gln 185	gga Gly	ccc Pro	698
gac Asp	ctt Leu	gaa Glu 190	ggg Gly	aag Lys	atg Met	gtt Val	cgc Arg 195	ttt Phe	gtt Val	tcg Ser	tct Ser	gca Ala 200	ggc Gly	tat Tyr	agt Ser	746
tca Ser	acg Thr 205	gtt Val	ttt Phe	tat Tyr	ggg Gly	gat Asp 210	cga Arg	aaa Lys	gtc Val	aca Thr	ctc Leu 215	tcg Ser	gtg Val	ggg Gly	aac Asn	794
act Thr 220	ctt Leu	ctg Leu	ttc Phe	aaa Lys	tat Tyr 225	gta Val	aat Asn	ggg Gly	cag Gln	tgg Trp 230	ttc Phe	cgc Arg	tcc Ser	ggg Gly	gaa Glu 235	842
ctg Leu	gag Glu	aat Asn	aat Asn	cga Arg 240	atc Ile	act Thr	tat Tyr	gct Ala	cag Gln 245	cat His	att Ile	tgg Trp	agt Ser	gct Ala 250	gaa Glu	890
ctg Leu	cct Pro	gcg Ala	cac His 255	tgg Trp	atc Ile	gtg Val	cct Pro	ggg Gly 260	tta Leu	aac Asn	ttg Leu	gtg Val	att Ile 265	aaa Lys	cag Gln	938
ggc Gly	aat Asn	ctg Leu 270	agc Ser	ggg Gly	cgc Arg	cta Leu	aat Asn 275	gat Asp	atc Ile	aag Lys	att Ile	gga Gly 280	gca Ala	ccg Pro	ggg Gly	986
gag Glu 285	ctg Leu	ttg Leu	ttg Leu	cat His	aca Thr	att Ile 290	gat Asp	atc Ile	ggg Gly	atg Met	ttg Leu 295	acc Thr	act Thr	ccc Pro	cgg Arg	1034
gat Asp 300	cgc Arg	ttt Phe	gat Asp	ttt Phe	gcc Ala 305	aaa Lys	gac Asp	aaa Lys	gaa Glu	gca Ala 310	cat His	agg Arg	gaa Glu	tat Tyr	ttc Phe 315	1082
cag Gln	acc Thr	att Ile	cct Pro	gta Val 320	agt Ser	cgt Arg	atg Met	att Ile	gtt Val 325	aat Asn	aat Asn	tat Tyr	gcg Ala	cct Pro 330	cta Leu	1130
cac His	cta Leu	aag Lys	gaa Glu 335	gtt Val	atg Met	tta Leu	cca Pro	acc Thr 340	gga Gly	gag Glu	tta Leu	ttg Leu	aca Thr 345	gat Asp	atg Met	1178
gat Asp	cca Pro	gga Gly 350	aat Asn	ggg Gly	ggg Gly	tgg Trp	cat His 355	agt Ser	ggg Gly	aca Thr	atg Met	cgt Arg 360	caa Gln	aga Arg	ata Ile	1226
ggg Gly 365	aaa Lys	gaa Glu	ttg Leu	gtt Val	tcg Ser	cat His 370	ggc Gly	att Ile	gat Asp	aat Asn	gct Ala 375	aac Asn	tat Tyr	ggg Gly	tta Leu	1274
aat Asn 380	agt Ser	acc Thr	gca Ala	ggc Gly	tta Leu 385	ggg Gly	gag Glu	aat Asn	agt Ser	cat His 390	cca Pro	tat Tyr	gta Val	gtt Val	gcg Ala 395	1322

## 096429-9141.ST25.txt

caa tta gcg gca cat aat agc cgc ggt aat tat gct aat ggc atc cag Gln Leu Ala Ala His Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln 400 405 410	1370
gtt cat ggt ggc tcc gga ggt ggg gga att gtt act tta gat tcc aca Val His Gly Gly Ser Gly Gly Gly Gly Ile Val Thr Leu Asp Ser Thr 415 420 425	1418
ttg ggg aat gag ttc agt cat gat gtt ggt cat aat tat ggt ctt ggt Leu Gly Asn Glu Phe Ser His Asp Val Gly His Asn Tyr Gly Leu Gly 430 435 440	1466
cat tat gta gat ggt ttc aag ggt tct gta cat cgt agt gca gaa aat His Tyr Val Asp Gly Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn 445 450 455	1514
aac aac tca act tgg gga tgg gat ggt gat aaa aaa cgg ttt att cct Asn Asn Ser Thr Trp Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro 460 465 470 475	1562
aac ttt tat ccg tct caa aca aat gaa aag agt tgt ctg aat aat cag Asn Phe Tyr Pro Ser Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln 480 485 490	1610
tgt caa gaa ccg ttt gat gga cac aaa ttt ggt ttt gac gcc atg gcg Cys Gln Glu Pro Phe Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala 495 500 505	1658
gga ggc agc cct ttc tct gct gca aac cgt ttc aca atg tat act ccg Gly Gly Ser Pro Phe Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro 510 515 520	1706
aat tca tcg gct atc atc cag cgt ttt ttt gaa aat aaa gct gtg ttc Asn Ser Ser Ala Ile Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe 525 530 535	1754
gat agc cgt tcc tcc acc ggc ttc agc aag tgg aat gca gat acg cag Asp Ser Arg Ser Ser Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln 540 545 550 555	1802
gaa atg gaa ccg tat gaa cac acc att gac cgt gcg gag cag att acg Glu Met Glu Pro Tyr Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr 560 565 570	1850
gct tca gtc aat gag cta agt gaa agc aaa atg gct gag ctg atg gca Ala Ser Val Asn Glu Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala 575 580 585	1898
gag tac gct gtc gtc aaa gtg cat atg tgg aac ggt aac tgg aca aga Glu Tyr Ala Val Val Lys Val His Met Trp Asn Gly Asn Trp Thr Arg 590 595 600	1946
aac atc tat atc cct aca gcc tcc gca gat aat aga ggc agt atc ctg Asn Ile Tyr Ile Pro Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu 605 610 615	1994
acc atc aac cat gag gcc ggt tat aat agt tat ctg ttt ata aat ggt Thr Ile Asn His Glu Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly 620 625 630 635	2042
gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp 640 645 650	2090



## 096429-9141.ST25.txt

ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg 655 660 665	2138
aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr 670 675 680	2186
gat ccg gaa ggc acg ctg tca agc tac atc tat cct gcg atg tat ggt Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly 685 690 695	2234
gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn 700 705 710 715	2282
gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg 720 725 730	2330
ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile 735 740 745	2378
aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn 750 755 760	2426
aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu 765 770 775	2474
acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly 780 785 790 795	2522
tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly 800 805 810	2570
caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val 815 820 825	2618
tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp 830 835 840	2666
aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro 845 850 855	2714
gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe 860 865 870 875	2762
agt aaa cct agg tca atg agg gtt gta tat aaa Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys 880 885	2795

&lt;211&gt; 886

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism: E. coli O157:H7 plasmid pO157

&lt;400&gt; 19

Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu Ala Pro Leu Ala Ile  
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Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe  
 20 25 30

Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu  
 35 40 45

Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly  
 50 55 60

Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val  
 65 70 75 80

Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg  
 85 90 95

Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser  
 100 105 110

Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly  
 115 120 125

Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val  
 130 135 140

Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser  
 145 150 155 160

His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg  
 165 170 175

Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys  
 180 185 190

Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr  
 195 200 205

Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys  
 210 215 220

Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg  
 225 230 235 240

Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp  
 245 250 255

Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly  
 260 265 270

Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His  
 275 280 285

Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe  
 290 295 300

Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val  
 305 310 315 320

Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val  
 325 330 335

Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met Asp Pro Gly Asn Gly  
 340 345 350

Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile Gly Lys Glu Leu Val  
 355 360 365

Ser His Gly Ile Asp Asn Ala Asn Tyr Gly Leu Asn Ser Thr Ala Gly  
 370 375 380

Leu Gly Glu Asn Ser His Pro Tyr Val Val Ala Gln Leu Ala Ala His  
 385 390 395 400

Asn Ser Arg Gly Asn Tyr Ala Asn Gly Ile Gln Val His Gly Gly Ser  
 405 410 415

Gly Gly Gly Gly Ile Val Thr Leu Asp Ser Thr Leu Gly Asn Glu Phe  
 420 425 430

Ser His Asp Val Gly His Asn Tyr Gly Leu Gly His Tyr Val Asp Gly  
 435 440 445

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Phe Lys Gly Ser Val His Arg Ser Ala Glu Asn Asn Asn Ser Thr Trp  
 450 455 460  
 Gly Trp Asp Gly Asp Lys Lys Arg Phe Ile Pro Asn Phe Tyr Pro Ser  
 465 470 475 480  
 Gln Thr Asn Glu Lys Ser Cys Leu Asn Asn Gln Cys Gln Glu Pro Phe  
 485 490 495  
 Asp Gly His Lys Phe Gly Phe Asp Ala Met Ala Gly Gly Ser Pro Phe  
 500 505 510  
 Ser Ala Ala Asn Arg Phe Thr Met Tyr Thr Pro Asn Ser Ser Ala Ile  
 515 520 525  
 Ile Gln Arg Phe Phe Glu Asn Lys Ala Val Phe Asp Ser Arg Ser Ser  
 530 535 540  
 Thr Gly Phe Ser Lys Trp Asn Ala Asp Thr Gln Glu Met Glu Pro Tyr  
 545 550 555 560  
 Glu His Thr Ile Asp Arg Ala Glu Gln Ile Thr Ala Ser Val Asn Glu  
 565 570 575  
 Leu Ser Glu Ser Lys Met Ala Glu Leu Met Ala Glu Tyr Ala Val Val  
 580 585 590  
 Lys Val His Met Trp Asn Gly Asn Trp Thr Arg Asn Ile Tyr Ile Pro  
 595 600 605  
 Thr Ala Ser Ala Asp Asn Arg Gly Ser Ile Leu Thr Ile Asn His Glu  
 610 615 620  
 Ala Gly Tyr Asn Ser Tyr Leu Phe Ile Asn Gly Asp Glu Lys Val Val  
 625 630 635 640  
 Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp Gly Gln Phe Trp Lys  
 645 650 655  
 Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg Lys Pro Glu Gln Phe  
 660 665 670  
 Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr Asp Pro Glu Gly Thr  
 675 680 685  
 Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly Ala Tyr Gly Phe Thr  
 690 695 700

096429-9141.ST25.txt

Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn Asp Cys Gln Leu Gln  
705 710 715 720

Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg Leu Ala Asn His Arg  
725 730 735

Ala Asn Asn Thr Val Met Asn Lys Phe His Ile Asn Val Pro Thr Glu  
740 745 750

Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn Asn Lys Ile Leu Asp  
755 760 765

Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu Thr Tyr Thr Val Asn  
770 775 780

Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly Cys Ile Val Ser Val  
785 790 795 800

Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly Gln Arg Ser Gly Tyr  
805 810 815

Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val Tyr Val Asp Ser Gly  
820 825 830

Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp Asn Leu Ser Tyr Asn  
835 840 845

Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro Ala Asp Met Lys Lys  
850 855 860

Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe Ser Lys Pro Arg Ser  
865 870 875 880

Met Arg Val Val Tyr Lys  
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<211> 37

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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<210> 21

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 21  
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<210> 22

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

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<210> 23

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<400> 23  
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide

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34

<210> 25

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 25

aaaaatggcc acgaagtggc cgcaccgtct cagg

34